RAW SEQUENCE LISTING   DATE: 10/11/2001
PATENT APPLICATION: US/09/807,470   TIME: 10:54:43

Input Set : A:\0020-4850P.ST25.txt
Output Set: N:\CRF3\10112001\I807470.raw

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 3 <110> APPLICANT: TOHDOH, Naoki et al.
 5 <120> TITLE OF INVENTION: NOVEL PROTEIN WAR-1 AND GENE THEREOF
 7 <130> FILE REFERENCE: 0020-4850p
 9 <140> CURRENT APPLICATION NUMBER: 09/807,470
10 <141> CURRENT FILING DATE: 2001-04-13
12 <160> NUMBER OF SEQ ID NOS: 13
14 <170> SOFTWARE: PatentIn version 3.0
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18 <212> TYPE: DNA
19 <213> ORGANISM: Rattus norvegicus
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30 ctgtgttgct atggtgatga tggcaatggt aatgacagtg gcaccagatt tccctgttcc       180
32 tgggaagccc ctccggctcc cgcgggtggg cggcggcggc gatcggtgcg gcaaatccgc       240
34 gctcgcaccc gggcctgcgg ggcaggggcg cggcgctcga tttccttccc tgcctctgca       300
36 gcccctgtgc gcatgctcgg cctacgcggc cccagccttt gattgatcgg tcggcagcgg       360
38 ctgcgaccct gggcggcaga cgggcgggga tggggagccc ggcgctggga gcggcgcagt       420
40 gatcagcggt ggcggccggt gagtaccggt gagtaccgcg gc atg ggg ctc cgc        474
41                                                  Met Gly Leu Arg
42                                                   1
44 aag aag aac gcc agg aac ccc ccg gtg ctg agc cac gaa ttc atg gtg       522
45 Lys Lys Asn Ala Arg Asn Pro Pro Val Leu Ser His Glu Phe Met Val
46  5                   10                  15                  20
48 cag aac cac gcg gat atg gtc tcc tgc gtg ggc atg ttc ttc gtg ctg       570
49 Gln Asn His Ala Asp Met Val Ser Cys Val Gly Met Phe Phe Val Leu
50                  25                  30                  35
52 gga ctt atg ttc gag ggc acg gcc gag atg tcg atc gtg ttc ctc acc       618
53 Gly Leu Met Phe Glu Gly Thr Ala Glu Met Ser Ile Val Phe Leu Thr
54                  40                  45                  50
56 ctg cag cat gga gtc gtt gtc cca gcg gaa ggg cta ccc tcg ggg tcc       666
57 Leu Gln His Gly Val Val Val Pro Ala Glu Gly Leu Pro Ser Gly Ser
58          55                  60                  65
60 agg acc ctt tac cat tat ggg gtc aaa gat ctg gcc aca gtg ttc ttc       714
61 Arg Thr Leu Tyr His Tyr Gly Val Lys Asp Leu Ala Thr Val Phe Phe
62      70                  75                  80
64 tac atg ctg gtg gcc atc atc att cac gcc acc att cag gag tac gtg       762
65 Tyr Met Leu Val Ala Ile Ile Ile His Ala Thr Ile Gln Glu Tyr Val
66 85                  90                  95                 100
68 cta gat aag ctc agc cgg aga ctg cag ctc acc aaa ggc aaa caa aac       810
69 Leu Asp Lys Leu Ser Arg Arg Leu Gln Leu Thr Lys Gly Lys Gln Asn
70                 105                 110                 115
72 aaa ttg aat gag gcc ggg cag ctg agt gtg ttc tac ata gtg tct ggt       858
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73 Lys Leu Asn Glu Ala Gly Gln Leu Ser Val Phe Tyr Ile Val Ser Gly
74 .           120             125             130
76 atc tgg ggt atg atc att ctg gcc tct gag aac tgc ctg tca gac ccc    906
77 Ile Trp Gly Met Ile Ile Leu Ala Ser Glu Asn Cys Leu Ser Asp Pro
78           135             140             145
80 act cta ttg tgg aag tct cag ccc cac aac atg atg aca ttt cag atg    954
81 Thr Leu Leu Trp Lys Ser Gln Pro His Asn Met Met Thr Phe Gln Met
82     150             155             160
84 aaa ttt ttc tac atc tca cag ttg gct tac tgg ttt cat agt ttc ccg    1002
85 Lys Phe Phe Tyr Ile Ser Gln Leu Ala Tyr Trp Phe His Ser Phe Pro
86 165             170             175             180
88 gag ctc tac ttc cag aaa gtc agg aaa caa gat atc ccg ggt caa ctc    1050
89 Glu Leu Tyr Phe Gln Lys Val Arg Lys Gln Asp Ile Pro Gly Gln Leu
90             185             190             195
92 atc tac att ggc ctc cac ctc ttc cac att gga ggg gcc tat ctc ttg    1098
93 Ile Tyr Ile Gly Leu His Leu Phe His Ile Gly Gly Ala Tyr Leu Leu
94           200             205             210
96 tac ttg aac cac ctg ggc ctg ctg ctt ctg atg ctg cac tat gct gtc    1146
97 Tyr Leu Asn His Leu Gly Leu Leu Leu Leu Met Leu His Tyr Ala Val
98           215             220             225
100 gag ctc ctc tcc agc gtg tgc agc ctg ctt tac ttt ggg gat gag cgg   1194
101 Glu Leu Leu Ser Ser Val Cys Ser Leu Leu Tyr Phe Gly Asp Glu Arg
102     230             235             240
104 tac cag aaa ggg ttg tct ttg tgg cct atc gtg ttt ata tcc ggg aga   1242
105 Tyr Gln Lys Gly Leu Ser Leu Trp Pro Ile Val Phe Ile Ser Gly Arg
106 245             250             255             260
108 ctc gtg aca ctg att gtc tca gtg gtt aca gta ggg ctt cac ttg gcc   1290
109 Leu Val Thr Leu Ile Val Ser Val Val Thr Val Gly Leu His Leu Ala
110             265             270             275
112 ggg aca aat cgg aat gga aat gct ctc tct ggt aat gtc aat gtg ttg   1338
113 Gly Thr Asn Arg Asn Gly Asn Ala Leu Ser Gly Asn Val Asn Val Leu
114           280             285             290
116 gca gct aaa atc gct gtt ctg tcc tcg agt tgc agt atc cag gtg tac   1386
117 Ala Ala Lys Ile Ala Val Leu Ser Ser Ser Cys Ser Ile Gln Val Tyr
118           295             300             305
120 ata aca tgg acc ttg acg acc gtc tgg ctt cag aga tgg tta gaa gat   1434
121 Ile Thr Trp Thr Leu Thr Thr Val Trp Leu Gln Arg Trp Leu Glu Asp
122     310             315             320
124 gcg aat ctt cat gtc tgt ggg agg aag aga cgg tcc agg tcg aga aaa   1482
125 Ala Asn Leu His Val Cys Gly Arg Lys Arg Arg Ser Arg Ser Arg Lys
126 325             330             335             340
128 ggc aca gaa aat gga gtg gag aat cca aat aga ata gat tct cca cca   1530
129 Gly Thr Glu Asn Gly Val Glu Asn Pro Asn Arg Ile Asp Ser Pro Pro
130             345             350             355
132 aag aag aaa gag aaa gct cct tag cagttgcaag cgaattgatt cttacctcca   1584
133 Lys Lys Lys Glu Lys Ala Pro
134             360
136 agggaatcca cttcttctta tgtggtgtct ctgtgctaga gattttctgt tcttcagaac   1644
138 gggtcgtgct ttttgaatat tgctaatgta ttgtctaatg tgtttttaag gttttgcaga   1704
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140 cgtatgagtg ggggatgggg gttaagacta aaccactcag cctctaaata cagtcagaat    1764
142 agttaacgga ccaacatctt atttagttag gttcttacct caacgatttt ccaaacgttt    1824
144 tgtggtgatg actgcagaat tgtgtacata aataatagtt tcctgcttcc aatgttcttt    1884
146 atcgaattaa caagtctgct agcaaagtgg tttgttttct caatgttctc ctgcaggata    1944
148 aagtggaaaa tctgataaag gttaaactca aatcagtatt atgtaaccgt tgggattttt    2004
150 ttaaagtgtt ttaaatttac aatggaaagc atttgtcaaa ccaccaaaaa tatgtgttta    2064
152 attttatgag tagtaattgt tagtgcttac gcccccatta aagcatcaaa atatgaatag    2124
154 atgacatgtg tggtgatatt gacatttagc gaatcaagat acctttaata aatatggtgg    2184
156 gttactaaag aagtaaacga cttcttcctg tttattttaa acacttgtac aggaaaactc    2244
158 gcaaaattaa atattactga aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa    2304
160 aaaaaaa                                                             2311
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164 <211> LENGTH: 363
165 <212> TYPE: PRT
166 <213> ORGANISM: Rattus norvegicus
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175             20                  25                  30
178 Phe Phe Val Leu Gly Leu Met Phe Glu Gly Thr Ala Glu Met Ser Ile
179             35                  40                  45
182 Val Phe Leu Thr Leu Gln His Gly Val Val Val Pro Ala Glu Gly Leu
183         50                  55                  60
186 Pro Ser Gly Ser Arg Thr Leu Tyr His Tyr Gly Val Lys Asp Leu Ala
187 65                  70                  75                  80
190 Thr Val Phe Phe Tyr Met Leu Val Ala Ile Ile Ile His Ala Thr Ile
191             85                  90                  95
194 Gln Glu Tyr Val Leu Asp Lys Leu Ser Arg Arg Leu Gln Leu Thr Lys
195             100                 105                 110
198 Gly Lys Gln Asn Lys Leu Asn Glu Ala Gly Gln Leu Ser Val Phe Tyr
199         115                 120                 125
202 Ile Val Ser Gly Ile Trp Gly Met Ile Ile Leu Ala Ser Glu Asn Cys
203     130                 135                 140
206 Leu Ser Asp Pro Thr Leu Leu Trp Lys Ser Gln Pro His Asn Met Met
207 145                 150                 155                 160
210 Thr Phe Gln Met Lys Phe Phe Tyr Ile Ser Gln Leu Ala Tyr Trp Phe
211                 165                 170                 175
214 His Ser Phe Pro Glu Leu Tyr Phe Gln Lys Val Arg Lys Gln Asp Ile
215             180                 185                 190
218 Pro Gly Gln Leu Ile Tyr Ile Gly Leu His Leu Phe His Ile Gly Gly
219         195                 200                 205
222 Ala Tyr Leu Leu Tyr Leu Asn His Leu Gly Leu Leu Leu Leu Met Leu
223     210                 215                 220
226 His Tyr Ala Val Glu Leu Leu Ser Ser Val Cys Ser Leu Leu Tyr Phe
227 225                 230                 235                 240
230 Gly Asp Glu Arg Tyr Gln Lys Gly Leu Ser Leu Trp Pro Ile Val Phe
231             245                 250                 255
234 Ile Ser Gly Arg Leu Val Thr Leu Ile Val Ser Val Val Thr Val Gly
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235              260              265              270
238 Leu His Leu Ala Gly Thr Asn Arg Asn Gly Asn Ala Leu Ser Gly Asn
239          275              280              285
242 Val Asn Val Leu Ala Ala Lys Ile Ala Val Leu Ser Ser Ser Cys Ser
243       290              295              300
246 Ile Gln Val Tyr Ile Thr Trp Thr Leu Thr Thr Val Trp Leu Gln Arg
247 305              310              315              320
250 Trp Leu Glu Asp Ala Asn Leu His Val Cys Gly Arg Lys Arg Arg Ser
251              325              330              335
254 Arg Ser Arg Lys Gly Thr Glu Asn Gly Val Glu Asn Pro Asn Arg Ile
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259          355              360
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264 <212> TYPE: DNA
265 <213> ORGANISM: Homo sapiens
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269 <222> LOCATION: (477)..(1586)
271 <400> SEQUENCE: 3
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276 tactaatgaa gatgccacta aaaaaaagaa ttcaggagca tcttggcggt ggcagcgagt     180
278 ttgaagatgc gacgatcaac gttgaagatc accgctcgca accccgggcc tggcgccggg     240
280 tagggcgcg gcgctcgatt tccttccctg cctccgccgt ccccctggtg cgcatgctca     300
282 gctcagctcg gccctcgcct ttgatttatt tttttctgg gcggccgctg cgacccggga     360
284 ctgacttcgg gatgggaagt ggagcccccg gagctgctac cgtggcggcg gcgctgtgag     420
286 gagcagccag ggggaggcag ctgcggctcg ccggtgagta tccgggaagc gccacc atg     479
287                                                                 Met
288                                                                  1
290 ggg ctc cgt aag aag agc acc aag aac ccc ccc gtt ctc agc cag gaa     527
291 Gly Leu Arg Lys Lys Ser Thr Lys Asn Pro Pro Val Leu Ser Gln Glu
292          5               10              15
294 ttc atc ctg cag aat cat gcg gac atc gtc tcc tgc gtg ggg atg ttc     575
295 Phe Ile Leu Gln Asn His Ala Asp Ile Val Ser Cys Val Gly Met Phe
296          20              25              30
298 ttc ctg ctg ggg ctt gtg ttc gag gga aca gca gaa gca tcc atc gtg     623
299 Phe Leu Leu Gly Leu Val Phe Glu Gly Thr Ala Glu Ala Ser Ile Val
300       35              40              45
302 ttt ctc act ctt cag cac agt gtt gct gtc cct gca gca gag gaa caa     671
303 Phe Leu Thr Leu Gln His Ser Val Ala Val Pro Ala Ala Glu Glu Gln
304 50              55              60              65
306 gcc acg ggc tca aag tcc ctc tat tat tat ggt gtc aaa gat ttg gcc     719
307 Ala Thr Gly Ser Lys Ser Leu Tyr Tyr Tyr Gly Val Lys Asp Leu Ala
308              70              75              80
310 acg gtt ttc ttc tac atg ctg gtg gca atc att att cat gcc aca att     767
311 Thr Val Phe Phe Tyr Met Leu Val Ala Ile Ile Ile His Ala Thr Ile
312          85              90              95
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314 cag gaa tat gtg ttg gat aaa att aac aag aga atg cag ttc acc aaa      815
315 Gln Glu Tyr Val Leu Asp Lys Ile Asn Lys Arg Met Gln Phe Thr Lys
316         100                 105                 110
318 gcg aaa caa aac aag ttt aac gag tct ggt cag ttt agt gtg ttc tac      863
319 Ala Lys Gln Asn Lys Phe Asn Glu Ser Gly Gln Phe Ser Val Phe Tyr
320     115                 120                 125
322 ttt ttt tct tgt att tgg ggc aca ttc att tta atc tct gaa aac tgc      911
323 Phe Phe Ser Cys Ile Trp Gly Thr Phe Ile Leu Ile Ser Glu Asn Cys
324 130                 135                 140                 145
326 ctg tca gac cca act ctt ata tgg aag gct cgt ccc cat agc atg atg      959
327 Leu Ser Asp Pro Thr Leu Ile Trp Lys Ala Arg Pro His Ser Met Met
328             150                 155                 160
330 aca ttt caa atg aag ttt ttc tac ata tcc cag ttg gct tac tgg ttt     1007
331 Thr Phe Gln Met Lys Phe Phe Tyr Ile Ser Gln Leu Ala Tyr Trp Phe
332         165                 170                 175
334 cat gct ttt cct gaa ctc tac ttc cag aaa acc aaa aaa caa gac atc     1055
335 His Ala Phe Pro Glu Leu Tyr Phe Gln Lys Thr Lys Lys Gln Asp Ile
336         180                 185                 190
338 cct cgt caa ctt gtc tac att ggt ctt cac ctc ttc cac att act gga     1103
339 Pro Arg Gln Leu Val Tyr Ile Gly Leu His Leu Phe His Ile Thr Gly
340     195                 200                 205
342 gct tat ctc ttg tac ttg aat cat ttg gga ctt ctt ctt ttg gta ctg     1151
343 Ala Tyr Leu Leu Tyr Leu Asn His Leu Gly Leu Leu Leu Leu Val Leu
344 210                 215                 220                 225
346 cat tat ttt gtt gaa tta ctt tcc cac atg tgc ggc ctg ttt tac ttt     1199
347 His Tyr Phe Val Glu Leu Leu Ser His Met Cys Gly Leu Phe Tyr Phe
348             230                 235                 240
350 agt gat gaa aag tac cag aaa ggc ata tct ctg tgg gcc att gtg ttt     1247
351 Ser Asp Glu Lys Tyr Gln Lys Gly Ile Ser Leu Trp Ala Ile Val Phe
352             245                 250                 255
354 atc ttg ggt aga ctt gtg act tta att gtt tcc gta ctc act gtt ggg     1295
355 Ile Leu Gly Arg Leu Val Thr Leu Ile Val Ser Val Leu Thr Val Gly
356         260                 265                 270
358 ttt cac ctg gct gga tcg cag aat cgg aat cct gat gcc ctt act gga     1343
359 Phe His Leu Ala Gly Ser Gln Asn Arg Asn Pro Asp Ala Leu Thr Gly
360     275                 280                 285
362 aat gta aat gtg ttg gca gct aaa att gct gtt ctg tcg tcc agt tgc     1391
363 Asn Val Asn Val Leu Ala Ala Lys Ile Ala Val Leu Ser Ser Ser Cys
364 290                 295                 300                 305
366 acg atc caa gcc tac gta aca tgg aac tta att act ctc tgg ctt cag     1439
367 Thr Ile Gln Ala Tyr Val Thr Trp Asn Leu Ile Thr Leu Trp Leu Gln
368             310                 315                 320
370 agg tgg gta gaa gat tct aat att cag gcc tca tgt atg aaa aag aaa     1487
371 Arg Trp Val Glu Asp Ser Asn Ile Gln Ala Ser Cys Met Lys Lys Lys
372             325                 330                 335
374 cgg tcg aga tct tct aaa aaa aga aca gaa aac gga gtg gga gtg gaa     1535
375 Arg Ser Arg Ser Ser Lys Lys Arg Thr Glu Asn Gly Val Gly Val Glu
376         340                 345                 350
378 act tca aat aga gta gac tgt ccg cca aag agg aaa gag aaa tct tca     1583
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